



N 0400
5-2-01.

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/829,066
Source: OIPF
Date Processed by STIC: 4/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/829,066

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 _____ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

Does Not Comply
Corrected Diskette Needed

ppr 1-3

4 <110> APPLICANT: Nisson, Paul
 5 Jesse, Joel
 6 Li, Wu-bo
 8 <120> TITLE OF INVENTION: Method for Isolating and Recovering Target DNA or RNA
 Molecules Having

9 a Desired Nucleotide Sequence
 11 <130> FILE REFERENCE: 0942.4800002
 W--> 14 <140> CURRENT APPLICATION NUMBER: US/09/829,066
 14 <141> CURRENT FILING DATE: 2001-04-10
 16 <150> PRIOR APPLICATION NUMBER: US 09/103,577
 17 <151> PRIOR FILING DATE: 1998-06-24
 19 <160> NUMBER OF SEQ ID NOS: 11
 21 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 23
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Oligonucleotide/Primer
 30 <220> FEATURE:
 31 <221> NAME/KEY: misc_feature
 32 <222> LOCATION: 3
 33 <223> OTHER INFORMATION: N is G, T, A, or C
 35 <220> FEATURE:
 36 <221> NAME/KEY: misc_feature
 37 <222> LOCATION: 6
 38 <223> OTHER INFORMATION: Y is C or T
 40 <220> FEATURE:
 41 <221> NAME/KEY: misc_feature
 42 <222> LOCATION: 9
 43 <223> OTHER INFORMATION: Y is C or T
 45 <220> FEATURE:
 46 <221> NAME/KEY: misc_feature
 47 <222> LOCATION: 12
 48 <223> OTHER INFORMATION: N is G, T, A, or C
 50 <220> FEATURE:
 51 <221> NAME/KEY: misc_feature
 52 <222> LOCATION: 15
 53 <223> OTHER INFORMATION: Y is C or T
 55 <220> FEATURE:
 56 <221> NAME/KEY: misc_feature
 57 <222> LOCATION: 18
 58 <223> OTHER INFORMATION: Y is C or T
 60 <220> FEATURE:
 61 <221> NAME/KEY: misc_feature
 62 <222> LOCATION: 21
 63 <223> OTHER INFORMATION: N is G, T, A, or C
 66 <400> SEQUENCE: 1
 W--> 67 gtnrtgygayg gntticyaygt nngg
 71 <210> SEQ ID NO: 2

(global error)
 invalid - Per 1.823 of sequence rules, the only valid
 <213> responses are: Unknown,
 Artificial Sequence, or
 Scientific name
 (Genus/species)
 (one of the three)
 see circled portion
 of Item 12 on Error
 Summary Sheet

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

```

72 <211> LENGTH: 19
73 <212> TYPE: DNA
74 <213> ORGANISM: Oligonucleotide/Primer
77 <400> SEQUENCE: 2
78 gtkttggaggk ttcagtkgg 19
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 18
84 <212> TYPE: DNA
85 <213> ORGANISM: Oligonucleotide/Primer
88 <400> SEQUENCE: 3
89 gtkttggaggk ttcagtgg 18
93 <210> SEQ ID NO: 4
94 <211> LENGTH: 18
95 <212> TYPE: DNA
96 <213> ORGANISM: Oligonucleotide/Primer
99 <400> SEQUENCE: 4
100 gtkttggaggk ttcagtkgg 18
104 <210> SEQ ID NO: 5
105 <211> LENGTH: 18
106 <212> TYPE: DNA
107 <213> ORGANISM: Oligonucleotide/Primer
111 <400> SEQUENCE: 5
112 gttggaggk ttcagtkgg 18
116 <210> SEQ ID NO: 6
117 <211> LENGTH: 17
118 <212> TYPE: DNA
119 <213> ORGANISM: Oligonucleotide/Primer
123 <400> SEQUENCE: 6
124 gttggaggk ttcagtgg 17
128 <210> SEQ ID NO: 7
129 <211> LENGTH: 17
130 <212> TYPE: DNA
131 <213> ORGANISM: Oligonucleotide/Primer
135 <400> SEQUENCE: 7
136 gtkttggaggk ttcagtgg 17
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 17
142 <212> TYPE: DNA
143 <213> ORGANISM: Oligonucleotide/Primer
147 <400> SEQUENCE: 8
148 gttggagggtt cagtkgg 17
152 <210> SEQ ID NO: 9
153 <211> LENGTH: 16
154 <212> TYPE: DNA
155 <213> ORGANISM: Oligonucleotide/Primer
157 <400> SEQUENCE: 9
158 gttggagggtt cagtgg 16
162 <210> SEQ ID NO: 10
163 <211> LENGTH: 25

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:24

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

164 <212> TYPE: DNA
165 <213> ORGANISM: Oligonucleotide/Primer
167 <400> SEQUENCE: 10
168 gaccgttcag ctggatatta cggcc
172 <210> SEQ ID NO: 11
173 <211> LENGTH: 13
174 <212> TYPE: DNA
175 ~~<213> ORGANISM: Oligonucleotide/Primer~~ → <220>
176 <223> OTHER INFORMATION: consensus sequence for initiation of translation
179 <400> SEQUENCE: 11
180 gccgccagcc aug

25

13

*insert this
mandatory
numeric
identifier
whenever
<221>, <222>,
or <223> is
shown.
<220> never
has a response;
it is a "header"
only.*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/829,066

DATE: 04/30/2001

TIME: 09:04:25

Input Set : A:\seqlist-09424800001.txt

Output Set: N:\CRF3\04302001\I829066.raw

L:14 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.

L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1